



- 1 -

SEQUENCE LISTING

<110> Willson, Tracey
Nicola , Nicos
Hilton, Douglas
Metcalf, Donald
Zhang , Jian

<120> A novel haemopoietin receptor and genetic sequences encoding same

<130> 23199-215

<140> US 09/688,286
<141> 2000-10-31

<150> AU PN6135
<151> 1995-10-23

<150> AU PN7276
<151> 1995-12-22

<150> AU PP2208
<151> 1996-09-09

<160> 12

<170> PatentIn version 3.1

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Thr Ala Thr Val Gly Gln Val Ala Ala Thr Glu Val Gln Pro Pro
20 25 30

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Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Ile Ile Trp
35 40 45

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Thr Trp Ser Pro Pro Glu Gly Ala Ser Pro Asn Cys Thr Leu Arg Tyr
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Phe Ser His Phe Asp Asp Gln Gln Asp Lys Lys Ile Ala Pro Glu Thr	
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cat cgt aaa gag gaa tta ccc ctg gat gag aaa atc tgt ctg cag gtg	348
His Arg Lys Glu Glu Leu Pro Leu Asp Glu Lys Ile Cys Leu Gln Val	
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Gly Ser Gln Cys Ser Ala Asn Glu Ser Glu Lys Pro Ser Pro Leu Val	
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aaa aag tgc atc tca ccc cct gaa ggt gat cct gag tcc gct gtg act	444
Lys Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val Thr	
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gag ctc aag tgc att tgg cat aac ctg agc tat atg aag tgt tcc tgg	492
Glu Leu Lys Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser Trp	
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ctc cct gga agg aat aca agc cct gac aca cac tat act ctg tac tat	540
Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr His Tyr Thr Leu Tyr Tyr	
145 150 155 160	
tgg tac agc agc ctg gag aaa agt cgt caa tgt gaa aac atc tat aga	588
Trp Tyr Ser Ser Leu Glu Lys Ser Arg Gln Cys Glu Asn Ile Tyr Arg	
165 170 175	
gaa ggt caa cac att gct tgt tcc ttt aaa ttg act aaa gtg gaa cct	636
Glu Gly Gln His Ile Ala Cys Ser Phe Lys Leu Thr Lys Val Glu Pro	
180 185 190	
agt ttt gaa cat cag aac gtt caa ata atg gtc aag gat aat gct ggg	684
Ser Phe Glu His Gln Asn Val Gln Ile Met Val Lys Asp Asn Ala Gly	
195 200 205	
aaa att agg cca tcc tgc aaa ata gtg tct tta act tcc tat gtg aaa	732
Lys Ile Arg Pro Ser Cys Lys Ile Val Ser Leu Thr Ser Tyr Val Lys	
210 215 220	
cct gat cct cca cat att aaa cat ctt ctc ctc aaa aat ggt gcc tta	780
Pro Asp Pro Pro His Ile Lys His Leu Leu Leu Lys Asn Gly Ala Leu	
225 230 235 240	
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Leu Val Gln Trp Lys Asn Pro Gln Asn Phe Arg Ser Arg Cys Leu Thr	
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tat gaa gtg gag gtc aat aat act caa acc gac cga cat aat att tta	876
Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn Ile Leu	
260 265 270	
gag gtt gaa gag gac aaa tgc cag aat tcc gaa tct gat aga aac atg	924
Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg Asn Met	
275 280 285	
gag ggt aca agt tgt ttc caa ctc cct ggt gtt ctt gcc gac gct gtc	972

Glu	Gly	Thr	Ser	Cys	Phe	Gln	Leu	Pro	Gly	Val	Leu	Ala	Asp	Ala	Val		
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gtc	gca	gtg	gca	gtc	ata	atc	ctc	ctt	ttt	tac	ctg	aaa	agg	ctt	aag	1164	
Val	Ala	Val	Ala	Val	Ile	Ile	Leu	Leu	Phe	Tyr	Leu	Lys	Arg	Leu	Lys		
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Ile	Ile	Ile	Phe	Pro	Pro	Ile	Pro	Asp	Pro	Gly	Lys	Ile	Phe	Lys	Glu		
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Gly	Ser	Gln	Cys	Ser	Ala	Asn	Glu	Ser	Glu	Lys	Pro	Ser	Pro	Leu	Val	100	105	110	
Lys	Lys	Cys	Ile	Ser	Pro	Pro	Glu	Gly	Asp	Pro	Glu	Ser	Ala	Val	Thr	115	120	125	
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Trp	Tyr	Ser	Ser	Leu	Glu	Lys	Ser	Arg	Gln	Cys	Glu	Asn	Ile	Tyr	Arg	165	170	175	
Glu	Gly	Gln	His	Ile	Ala	Cys	Ser	Phe	Lys	Leu	Thr	Lys	Val	Glu	Pro	180	185	190	
Ser	Phe	Glu	His	Gln	Asn	Val	Gln	Ile	Met	Val	Lys	Asp	Asn	Ala	Gly	195	200	205	
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Tyr Glu Val Glu Val Asn Asn Thr Gln Thr Asp Arg His Asn Ile Leu
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Glu Val Glu Glu Asp Lys Cys Gln Asn Ser Glu Ser Asp Arg Asn Met
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Glu Gly Thr Ser Cys Phe Gln Leu Pro Gly Val Leu Ala Asp Ala Val
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Tyr Thr Val Arg Val Arg Val Lys Thr Asn Lys Leu Cys Phe Asp Asp
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Asn Lys Leu Trp Ser Asp Trp Ser Glu Ala Gln Ser Ile Gly Lys Glu
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Gln Asn Ser Thr Phe Tyr Thr Thr Met Leu Leu Thr Ile Pro Val Phe
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Val Ala Val Ala Val Ile Ile Leu Leu Phe Tyr Leu Lys Arg Leu Lys
355 360 365

Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe Lys Glu
370 375 380

Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys Tyr Asp
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Ala Gly Gly Gly Gly Gly Gly Gly Gly Ala Pro Thr Glu Thr Gln Pro	
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Pro Val Thr Asn Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile	
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tgg aca tgg aat cca ccc gag gga gcc agc tca aat tgt agt cta tgg	252
Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp	
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Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu	
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Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln	
85 90 95	
gtg ggg tcc cag tgt agc acc aat gag agt gag aag cct agc att ttg	396
Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu	
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gtt gaa aaa tgc atc tca ccc cca gaa ggt gat cct gag tct gct gtg	444
Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val	
115 120 125	
act gaa ctt caa tgc att tgg cac aac ctg agc tac atg aag tgt tct	492
Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser	
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Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr	
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Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe	
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aga gaa ggc caa tac ttt ggt tgt tcc ttt gat ctg acc aaa gtg aag	636
Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys	
180 185 190	
gat tcc agt ttt gaa caa cac agt gtc caa ata atg gtc aag gat aat	684
Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile Met Val Lys Asp Asn	
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Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser Arg	
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225 230 235 240	
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Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg Cys	
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cta ttt tat gaa gta gaa gtc aat aac agc caa act gag aca cat aat	876
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Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val Pro	
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355 360 365	
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Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe	
370 375 380	
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Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys	
385 390 395 400	
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Tyr Asp Ile Tyr Glu Lys Gln Thr Lys Glu Glu Thr Asp Ser Val Val	
405 410 415	
ctg ata gaa aac ctg aag aaa gcc tct cag tgatggagat aatttatattt	1358
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Trp Thr Trp Asn Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp
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Tyr Phe Ser His Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu
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Thr Arg Arg Ser Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln
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Val Gly Ser Gln Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu
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Val Glu Lys Cys Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val
 115 120 125

Thr Glu Leu Gln Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser
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Trp Leu Pro Gly Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr
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Tyr Trp His Arg Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe
 165 170 175

Arg Glu Gly Gln Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys
 180 185 190

Asp Ser Ser Phe Glu Gln His Ser Val Gln Ile Met Val Lys Asp Asn
195 200 205

Ala Gly Lys Ile Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser Arg
210 215 220

Val Lys Pro Asp Pro Pro His Ile Lys Asn Leu Ser Phe His Asn Asp
225 230 235 240

Asp Leu Tyr Val Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg Cys
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Leu Phe Tyr Glu Val Glu Val Asn Asn Ser Gln Thr Glu Thr His Asn
260 265 270

Val Phe Tyr Val Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg
275 280 285

Asn Val Glu Asn Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp
290 295 300

Thr Leu Asn Thr Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr
305 310 315 320

Glu Asp Asp Lys Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly
325 330 335

Lys Lys Arg Asn Ser Thr Leu Tyr Ile Thr Met Leu Leu Ile Val Pro
340 345 350

Val Ile Val Ala Gly Ala Ile Ile Val Leu Leu Leu Tyr Leu Lys Arg
355 360 365

Leu Lys Ile Ile Ile Phe Pro Pro Ile Pro Asp Pro Gly Lys Ile Phe
370 375 380

Lys Glu Met Phe Gly Asp Gln Asn Asp Asp Thr Leu His Trp Lys Lys
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Glu Val Gln Pro Pro Val Thr Xaa Leu Ser Val
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Glu Val Gln Pro Pro Val Thr Xaa Leu Ser Val
20 25

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<223> peptide motif found in many members of the haemopoietin receptor family

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1 5